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Microbiome of athletes: Its features and diversity: A literature review

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Abstract. The microbiome of athletes is of the greatest interest among researchers, as the microbial composition of the colon plays a key role in the absorption of nutrients, the synthesis of vitamins, and the immune response of the host body. The purpose of this review was to investigate the relationship between the gut microbiota in high-performance athletes and people with low-activity lifestyles, and the effect of these changes on the production of microbial metabolites that are associated with physical performance and athletic performance of athletes. A total of 42 research papers were analysed, including 11 specialised studies that examined the effect of intense physical activity of different types on the microbial composition of the gut and 19 studies that focused on the correlation of individual bacteria and physical performance. Gut microbial composition has been found to be associated with athletic performance and is likely to improve performance and recovery. Physical activity has been shown to increase α-diversity and microbial metabolites, such as short-chain fatty acids, compared to people who have a low-activity lifestyle. There were no significant differences in α-diversity between sports. The microbiome of athletes was characterised by a higher amount of short-chain fatty acids, which can be energy substrates during exercise. The production of short-chain fatty acids is associated with *Eubacterium rectale, Blautia* spp., *Faecalibacterium prausnitzii*. The athletes' microbiome also demonstrated the presence of *Prevotella* spp., which in athletes may correlate with performance. It has been shown that the presence of *Veillonella atypica* in athletes positively correlates with endurance. Despite the fact that the findings are contradictory, sports achievements and health of athletes specialising in various sports are associated with such types of bacteria as *Akkermansia municiphila, Faecalibacterium prausnitzii, Eubacterium rectale, Roseburia hominis*. In addition, it has been shown that there is a link between the microbial composition of the gut and enzymes that are considered key in the production of metabolites associated with the health of athletes

Keywords: microbial composition; short-chain fatty acids; *Akkermansia*; *Veillonella atypica*; sporting achievements

Introduction

The microbial composition of the human gut is currently one of the key areas of research, especially in sports medicine, as it contains a huge potential for the health and adaptation of athletes. F. Fontana *et al.* [1] found that the lifestyle of athletes, namely the amount of training combined with nutrition, modulates the gut microbiota, thereby increasing the enzymatic capabilities of the host body, which affects muscle performance. A.E. Mohr *et al.* [2] confirmed that the human gut microbiota has a great metabolic potential and contains not only thousands of taxa of various bacteria, but also microbes, viruses, archaea and, most importantly, more than three million genes, affecting the immune system,

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the absorption of nutrients, and the synthesis of certain vitamins. Moreover, the microbial composition of athletes is significantly different from the microbial composition of people who have a low-activity lifestyle. Athletes have a significantly higher α-diversity of the microbiome, and a higher number of bacteria that are associated with health. R.L. Hughes & H.D. Holscher [3] found that working with the composition of the microbiota can be a strategy for improving athletic performance, as it promotes the health of the gastrointestinal tract, and therefore, the absorption of nutrients, and is also a producer of short-chain fatty acids (SCFA), which can be energy substrates, increasing the endurance of athletes. M.T. O'Brien *et al.* [4] note that probiotics, such as *Lactobacillus* spp. and *Bifidobacterium* spp. have a protective effect against upper respiratory tract infections, which often occur in elite athletes due to the immunosuppressive effect of high-intensity physical activity. K. Mańkowska *et al.* [5] concluded that the metabolism of certain nutrients occurs with the participation of the gut microbiota. In addition, *Bifidobacterium* spp. have a protective anti-inflammatory function. To confirm the anti-inflammatory function, H.Y. Cheng *et al.* [6] found that microorganisms that are part of the human gut microbiome can interfere with the colonisation of pathogens by stimulating the production of IL-10, IL-17, and IL-22, which are antimicrobial peptides. It has been confirmed that thousands of microorganisms from various phyla, such as *Firmicutes*, *Bacteroidetes*, Actinobacteria, and *Proteobacteria*, activate the body's protective functions, preventing the development of pathogens. Moreover, M. Parizadeh & C. Arrieta [7] note that the microbiome can potentially be used in therapeutic interventions, such as faecal transplantation, pro- and prebiotic implantation. M.J.W. Furber *et al.* [8] concluded that it is the stability of the gut microbiota that can improve athletic performance. R.L. Hughes [9] also found that the gut microbiome can have a significant impact on athletic performance by producing SCFA, using lactate, and inducing enzyme activity. The predominance of bacteria in the microbial composition of the intestines of athletes, which are associated with a high level of SCFA production, can contribute to athletic achievements in endurance sports, as noted by O. Palladina [10] and G. Baldanzi *et.al.* [11]. The effect of certain microorganisms on athletic performance was investigated by J. Scheiman *et al.* [12] and it was found that *Veillonella* spp., which was found in samples of intestinal microbiome of marathon runners, significantly contributes to the endurance of athletes. The available data indicate a significant potential for the gut microbiome to improve endurance and athletic performance. So far, researchers have investigated the functions of individual microorganisms and changes in microbial composition during dietary interventions. The purpose of this study was to systematise the general and distinctive features of the microbial composition of the intestine of both high-performance athletes specialising in various sports, and in comparison with individuals who have a low-activity lifestyle.

The literature search was carried out for the keywords "gut microbiome", "athletes' microbiome", "athletes' microbiota", "athletes' gut microbiota" in such databases as Medline (PubMed), Scopus (Elsevier), Google Scholar, Plos One. Data analysis was performed in accordance with the recommendations for meta-analysis [13]. Only randomised controlled trials, meta-analyses, and systematic reviews published between 2017 and 2024 were considered. 42 research papers were found. The criteria for inclusion in the analysis of the first division were studies on people (n>4 in each group) who were professionally engaged in sports. The second subsection included scientific sources that considered the effects of individual bacteria on physical performance.

The Difference Between the Microbiome of Athletes and People who do not Exercise

The results of studies that were conducted between 2017 and 2024 were compared (and also included a paper published in 2014, as the results became the basis for future research), the conclusions are set out in Table 1. It has been shown that there are significant differences between the microbiota of athletes and the microbiota of people who have a physically inactive lifestyle [14-16]. A greater α-diversity of microbiota was recorded in athletes, while the level of microorganisms of the *Bacteroidetes* phylum was reduced. Both athletes and people who have an active lifestyle are dominated by bacteria such as *Akkermansiaceae* and *Faecalibacterium* spp. [10, 17].

Table 1. Composition of the gut microbiota of athletes depending on the sport or in comparison with non-athletes

	Subjects	Year	Method	Features of the microbiota	Source
1	Various sports with aerobic and anaerobic loads (in particular, cyclists and rugby players) (n = 186)	2023	Shotgun metagenomic sequencing	*Eubacterium rectale*, *Blautia* spp., *Faecalibacterium prausnitzii*, etc. unclassified species of *Faecalibacterium*, *Ruminococcus bromii*, unclassified species of *Eubacterium* and *Ruminococcus*.	1
2	Irish athletes (n = 27) in 16 different sports	2020	Shotgun metagenomic sequencing	No differences in microbial composition were established depending on the sport. The samples were dominated by species of one or a combination of five species: *Gordonibacter massiliensis, Eubacterium rectale, Faecalibacterium prausnitzii, Bacteroides vulgatus*, and *Polynucleobacter necessarius*. Microbiota of athletes who specialised in dynamic sports (such as field hockey) was dominated by *Bifidobacterium animalis*, *Lactobacillus acidophilus, Prevotella intermedia*, and *F. prausnitzii*. Microbiota of athletes in sports that combine both dynamism and static (such as rowing) had higher amounts of *Bacteroides caccae.*	18

Continued Table 1

	Subjects	Year	Method	Features of the microbiota	Source
3	Male non-athletes (control group n = 10), bodybuilders (n = 15), runners (n = 15)	2019	Amplification of the 16S rRNA gene in the V3 and V4 regions	α and β diversity did not differ in different types of sports. Bodybuilders had the highest levels of *Faecalibacterium* spp., *Sutterella* spp., *Clostridium* spp., *Haemophilus* spp., and *Eisenbergiella* spp.	19
4	Athletes in endurance sports (n = 15), athletes in power sports (n = 16), control group (n = 21)	2024	Amplification of the 16S rRNA gene	No significant differences were found in α- and β- diversity between groups. In endurance athletes, the enterotype with *Bacteroide* spp. *s* dominated, while in strength athletes, the enterotype with *Prevotella* spp. prevailed. Positive correlations were found between SCFA producers (*Blautia wexlerae, Eubacterium rectale*, and *Intestinimonas timonensis*) and maximum power during the Wingale anaerobic test.	20
5	Rugby players (n = 40) and non-athletes with a BMI within the normal range (n = 46)	2014	Amplification of the 16S rRNA gene in the V4 region	Higher proportion of *Akkermansia* spp. compared to the control group.	21
6	Rugby players (n = 40) and non-athletes with a BMI within the normal range (n = 46)	2018	Shotgun metagenomic sequencing	Greater diversity of the athletes' microbiota compared to the control group. Higher number of SCFA.	22
7	Professional cyclists (n = 22) and amateur cyclists (n = 11)	2017	Shotgun metagenomic sequencing and RNA sequencing	No correlations were found between taxonomic groups. Higher relative abundance of *Prevotella* spp., depending on the number of training sessions (> 11 hours/week). Increased number of *Methanobrevibacter smithii* transcripts in professional athletes and low number of Bacteroides. 30 out of 33 athletes had *Akkermansia* spp.	23
8	Marathon athletes (n = 15) and subjects who have a sedentary lifestyle (n = 10)	2019	16S rDNA sequencing	Increase in the relative number of representatives of the genus *Veillonella* in athletes after the marathon.	12
9	Martial artists (n=31)	2019	Amplification of the 16S rRNA gene in the V3 and V4 regions	*Parabacteroides* spp., *Phascolarctobacterium* spp., *Oscillibacter* spp., and *Bilophila* spp. prevailed in higher-level athletes. *Megasphaera* spp. prevailed in lower-level athletes.	24
10	Marathon runners (n=14), skiers (n=11), control group (n=46)	2020	Amplification of the 16S rRNA gene	High ratio of *Prevotella* spp. to *Bacteroides* spp.	25
11	Triathletes (n=4), control group – healthy men with a BMI within the normal range (n=4)	2023	Microbial DNA sequencing	More α-diversity in athletes, and reduced levels of *Bacteroidetes*, increased levels of *Akkermansiaceae, Faecalibacterium* spp.	10

Source: compiled by the authors based on the data shown in the Table

Establishing a causal relationship between sports and the microbiome of athletes is quite problematic. The results can be influenced by environmental factors, dietary interventions, antibiotic use, differences in the intensity of physical training and its duration, methods of preparation and logistics of samples, databases, and bioinformatics methods [26, 27].

S.F. Clarke *et al.* [21] studied rugby athletes and found that they had a higher proportion of representatives of *Akkermansia* spp., compared to the control groups. The researchers note that dietary interventions, especially protein intake, may have affected an increase in the diversity of gut microbial composition. W. Barton *et al.* [22] continued their research by examining the samples using the shotgun metagenomic sequencing method. Their task was to understand the metabolic capacity and taxonomic composition. As a result, when studying the differences between the group of athletes and the control group, people who have an inactive lifestyle, more differences were demonstrated at the metabolic and metagenomic levels compared to the level of the gut microbiota. In addition, athletes were found to have higher amounts of short-chain fatty acids, particularly butyrate, propionate, and acetate, and increased ability of carbohydrate metabolism, protein synthesis, and other metabolic pathways compared to the control group.

L.M. Petersen *et al.* [23] analysed the difference in microbiota depending on the level of athletes. Although no significant correlations were found between taxonomic groups, however, the amount of exercise positively correlated with the abundance of *Prevotella* spp. In addition, professional cyclists had an increased number of *Methanobrevibacter smithii* transcripts compared to amateur cyclists and the low number of Bacteroides. In 30 of the 33 athletes *Akkermansia* spp. were isolated, which is usually associated with a healthier metabolic profile [28].

C.M. O'Donovan *et al.* [18], when studying differences in the quantitative composition of health-related bacteria among high-performance athletes specialising in various sports, found that there were no differences in microbial composition, depending on the sport. However, such spesies as *Gordonibacter massiliensis, Eubacterium rectale, Faecalibacterium prausnitzii, Bacteroides vulgatus, Polynucleobacter necessarius* were observed in samples. The species were either present in relatively equal quantities or exhibited a predominance of one over the others. It was also shown that athletes who specialised in more dynamic sports (such as field hockey) were higher numbers of likely to have *Bifidobacterium animalis, Lactobacillus acidophilus, Prevotella intermedia and F. prausnitzii,* while athletes in sports that combine both dynamism and static (such as rowing) correlated with higher numbers of *Bacteroides caccae.* In a study involving bodybuilders and athletes-runners, it was shown that α and β diversity did not differ in different types of sports. Bodybuilders had the highest levels of *Faecalibacterium* spp.*, Sutterella* spp.*, Clostridium* spp.*, Haemophilus* spp. *and Eisenbergiella* spp. [19].

R. Liang *et al.* [24] observed athletes specialising in martial arts at various competitive levels. Athletes of the highest competitive level had the prevalence of *Parabacteroides* spp.*, Phascolarctobacterium* spp.*, Oscillibacter* spp. and *Bilophila* spp., while the second group of athletes belonging to a lower competitive level had a higher number of *Megasphaera* spp. Separately, the training volume was monitored, i.e., the amount of time that participants trained during the average week. Increased training volume was positively correlated with the abundance of *Parabacteroides* spp.

M. Kulecka *et al.* [25] found that marathon runners and healthy non-athletes (control group) differed in 20 bacterial taxa, while the difference between skiers and the control group was 5 taxa. Both groups of athletes had low levels of the main genus of gut microbiota, *Bacteroidetes*, and a larger number of *Prevotella* spp. In addition, a greater diversity of the microbiome was inherent in athletes-skiers, compared with the control group, people who have an inactive lifestyle. Microbial composition was also found to correlate with the participants' diet. Folic acid intake increased the amount of *Christensenellaceae*, fibre positively correlated with *Agathobacter* spp., sucrose reduced the amount of *Prevotella* spp., and polyunsaturated fatty acids were inversely correlated with *Phascolarctobacterium* spp.

Published in 2024, the results of a study of the microbiome of athletes did not reveal significant differences in α and β-differences between the control group, the strength sports group, and the endurance sports group. Enterotype *Bacteroides* was predominant in athletes specialising in endurance sports, while *Prevotella* enterotype was common in athletes in strength sports. *Blautia wexlerae, Eubacterium rectale* and *Intestinimonas timonensis*, the main producers of SCFA, positively correlated with maximum power during the Wingale anaerobic test. It is important to note that SCFA can be used as an additional energy substrate, which is necessary for endurance sports [20].

It was shown that the microbial composition of the intestines of athletes is significantly more abundant and higher in α-diversity compared to subjects who have and a physically inactive, although there is no difference in diversity of intestinal bacteria, depending in the sport. The microbiome of athletes is dominated by producers of short-chain fatty acids, such as *Blautia wexlerae*, *Eubacterium rectale* and *Intestinimonas timonensis* related to health, and with greater energy potential. In addition, *Akkermansiaceae* and *Faecalibacterium* spp. significantly predominate in athletes and the number of *Bacteroidetes* is reduced, which signals the possibility of adaptation and endurance.

Potential Mechanisms of Microbiome Influence on Physical Performance

It has been found that the microbial composition of the intestines can potentially affect endurance, adaptability, and athletic performance. As already mentioned, athletes have predominantly *Akkermansia municiphila*, *Faecalibacterium prausnitzii, Eubacterium rectale, Roseburia hominis*, which are associated with sports results [15]. The presence of *Prevotella* spp. signals better results in power sports, while the predominance of SCFA producers *Blautia wexlerae, Eubacterium rectale* and *Intestinimonas timonensis* can improve results in endurance sports [20].

K. Gross *et al.* [29] demonstrated that a microbial-mediated mechanism can affect the ability to exercise endurance. Analysis of samples provided by marathon athletes 5 days before and after the marathon showed a significant increase in the relative numbers of *Veillonella* spp. for athletes after the marathon. *Veillonella* is a Gram-negative bacterium that uses lactate as its main source of energy, given that marathon running is characterised by a high level of lactate production by skeletal muscles. Later, a human strain of *Veillonella atypica* was isolated and it was demonstrated in an experiment on mice that this strain increased the time on the treadmill while the mice performed tasks. Further experiments have shown that lactate can enter the intestines, where it is catabolised by *Veillonella atypica* and it is converted to short-chain fatty acid propionate [12].

Metagenomic samples of athletes (shotgun sequencing) specialising in various sports were analysed and it was found that athletes have a greater variety of species of microbes that produce short-chain fatty acids, compared with the control group of subjects who have a sedentary lifestyle. Indeed, evidence suggests that physical activity increases α-diversity and microbial metabolites, such as short-chain fatty acids [14, 30, 31]. The latter are energy substrates during endurance exercise [32, 33]. This includes *Eubacterium rectale, Blautia* spp., *Faecalibacterium prausnitzii* and other unclassified species *Faecalibacterium*, *Ruminococcus bromii*. These taxa of bacteria are considered to be the "core" of producers of short-chain fatty acids. The athletes' microbiome also demonstrated the presence of *Prevotella* spp., or rather a dominant species *Prevotella copri.* In the control group, the presence of *Prevotella* spp. although was associated with the presence of inflammatory diseases in non-athletes, its presence may be correlated with performance in athletes [1].

It has been found that the microbial composition of the gut can affect the health of the host. The microbiota of the gastrointestinal tract promotes the absorption of nutrients and the synthesis of vitamins, which is extremely important, since physical activity can increase the rate of energy metabolism in skeletal muscles from 20 to 100 times [34-36]. The connection between the microbe and the modulation of inflammation and the body's immune response is also known [37-39]. Moreover, the results of recent studies confirm the correlation between the athletic performance of athletes and the composition of their microbiota [10-12].

It was found that despite the great scientific interest in the topic of the athlete microbiome, the available scientific literature mainly focuses on a limited range of bacteria that are well studied. Research focuses on the products of key metabolites, in particular, short-chain fatty acids, lactate, and the involvement of association with dietary interventions. Until now, little is known about the physiological mechanisms involved in resident bacteria that are modulated by physical activity and their impact on the host in terms of physical performance and overall health. Only one paper has investigated the relationship between enzymes associated with the synthesis of metabolites that promote host health and the composition of the microbiome inherent in athletes. The researchers identified a number of enzymes associated with antibacterial properties, vitamin synthesis, reduced risk of cardiovascular diseases, energy metabolism, and antioxidant properties (Table 2). These findings confirm that athletes' microbiota can potentially encode a much wider range of microbial metabolites than is currently known, with important effects on health and physical performance.

Table 2. Cluster of enzymes that correlates with the microbiome inherent in athletes

Enzyme	Final product function
Spermidine synthase	Reducing the risk of CVD mortality
Porphobilinogen synthase	Heme synthesis
Mycothiol synthase	Antibacterial and antitumor properties
Hydrogenobyrinic acid a,c-diamide synthase	Biosynthesis of coenzyme B12 (cobalamin)
Cystathionine gamma synthase	Energy metabolism, muscle function, antioxidant
Glutamate synthase (NADPH), Glutaminyl-tRNA synthase	Excitatory neurotransmitter, homocysteine balance

Source: [1]

Studies of the microbiome of athletes have certain limitations that need to be considered in the further studies. The individual microbial composition of the intestine is affected by dietary interventions, the volume and intensity of training, changing the location, taking antibiotics and other medications. The results are also influenced by the samples and their number, and the methodology chosen by researchers. In addition, it is necessary to consider the possibilities of individual variations in the microbiome of athletes, for example, with the help of probiotics. Probiotics have been shown to promote the absorption of branched-chain amino acids, and increase the amount of glycogen in the muscles and liver [40]. The gut microbiome has also been shown to accelerate erythropoiesis, so researchers have suggested that probiotic supplementation may improve athletic performance in sports with aerobic muscle energy [41]. However, the results of the study do not confirm such conclusions, which most likely indicates the compensatory mechanisms of the athlete's body [42]. Studies show that physical activity increases the diversity of the microbiome and the number of metabolites important for physical performance. However, there are still many unknown aspects of the microbiota's impact on athletes' health and physical performance.

Conclusions

The authors set out to analyse the available studies published in the period 2017-2024, and to make a comparative analysis of the microbial composition of the intestines of athletes specialising in various sports, people having a low-activity lifestyle, and to establish how changes in the microbiome due to physical exertion can affect athletic performance, adaptive capabilities, and endurance of athletes.

The microbiota of athletes does not have a significant difference in α-diversity between sports, but it differs from the microbiota of non-athletes. The *Akkermansiaceae* and *Faecalibacterium* spp. significantly predominate in athletes. Reduced numbers of *Bacteroidetes* have been shown in athletes, signalling adaptability and endurance capabilities, although other studies have found that endurance athletes had a dominant *Bacteroides* enterotype, and strength athletes had a dominant *Prevotella* enterotype, which may correlate with performance in athletes. Elite rugby players were found to have higher amounts of short-chain fatty acids, such as butyrate, propionate, and acetate, and increased ability to metabolise carbohydrates, protein synthesis, and other metabolic pathways compared to the control group. Short-chain fatty acids can be used as energy substrates and are important in endurance sports. They are usually associated with *Eubacterium rectale, Blautia* spp., *Faecalibacterium prausnitzii.* In addition, in some studies, the microbiome of athletes showed a higher proportion of *Akkermansia* spp., which is usually associated with a healthy metabolic profile. The amount of exercise was positively correlated with a larger numbers of *Prevotella* spp., which in athletes may correlate with performance, since this bacterium uses lactate as an energy source. An increase in the numbers of *Veillonella* spp. in athletes after a marathon was shown. This bacterium is associated with the highest endurance of athletes, as it uses lactate as an energy source. A positive correlation was also found between the production of enzymes associated with the synthesis of metabolites that contribute to host health and the composition of the microbiome inherent in athletes. These enzymes are associated with antibacterial properties, vitamin synthesis, reduced risk of cardiovascular diseases, energy metabolism, and antioxidant properties.

The practical significance of this study is the identification of specific bacteria inherent in high-performance athletes to develop various interventions that will correct the intestinal microbial composition of athletes to enhance adaptive capabilities, endurance and improve athletic performance. Further research with a larger sample of athletes is required, considering other factors that may influence the outcome, such as weight changes, diet, and training periods.

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None.

Conflict of Interest

The authors declare no conflict of interest.

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Мікробіом спортсменів: його особливості і різноманіття: огляд літератури

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Анотація. Мікробіом спортсменів викликає найбільший інтерес серед дослідників, так як мікробний склад товстого кишківника відіграє ключову роль у засвоєнні нутрієнтів, синтезі вітамінів та імунній відповіді організму хазяїна. Метою даного огляду було вивчити зв'язок між кишковою мікробіотою у спортсменів вищих досягнень та людей із малоактивним способом життя, а також вплив цих змін на продукцію мікробних метаболітів, які пов›язані з фізичною працездатністю та спортивними досягненнями атлетів. Було проаналізовано 42 дослідження, з яких 11 спеціалізованих досліджень, які вивчали вплив інтенсивних фізичних навантажень різних видів на мікробний склад кишківника та 19 наукових робіт, які фокусувались на кореляції окремих бактерій та фізичної працездатності. Було виявлено, що мікробний склад кишківника пов'язаний зі спортивними результатами, і, вірогідно, може підвищувати продуктивність та відновлення. Було показано, що фізичні навантаження збільшують α-різноманітність і мікробні метаболіти, такі як коротколанцюгові жирні кислоти, порівняно з людьми, які ведуть малоактивний спосіб життя. Не було виявлено суттєвої відмінності у α-різноманітності між видами спорту. Мікробіом атлетів відрізнявся вищою кількістю коротколанцюгових жирних кислот, які можуть бути енергетичними субстратами при фізичних навантаженнях. Продукцію коротколанцюгових жирних кислот пов›язують з *Eubacterium rectale, Blautia* spp., *Faecalibacterium prausnitzii*. Мікробіом атлетів також продемонстрував наявність *Prevotella* spp., яка у спортсменів може корелювати з продуктивністю. Було показано, що наявна у атлетів *Veillonella atypica* позитивно корелює з витривалістю. Незважаючи на те, що результати досліджень є суперечливими, спортивні досягнення та здоров´я атлетів, що спеціалізуються у різних видах спорту, пов´язують з таким видами бактерій як *Akkermansia municiphila, Faecalibacterium prausnitzii, Eubacterium rectale, Roseburia hominis*. Окрім того, було показано, що існує зв´язок між мікробним складом кишківника та ферментами, які вважаються ключовими у продукції метаболітів, що пов›язані із здоров'ям спортсменів

Ключові слова: мікробний склад; коротколанцюгові жирні кислоти; *Akkermansia*; *Veillonella atypica*; спортивні досягнення